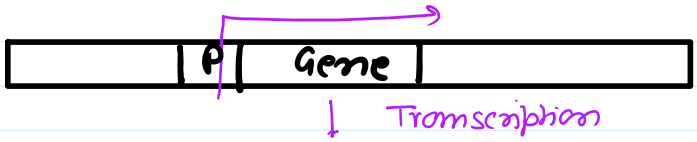
Transcription



↓ Transcription

RNA

- Adapter molecule → eg- t RNA
- Protein Synthesis → mRNA
- Catalytic Role → ↓
  - Type I & II Introns
  - Ribozyme

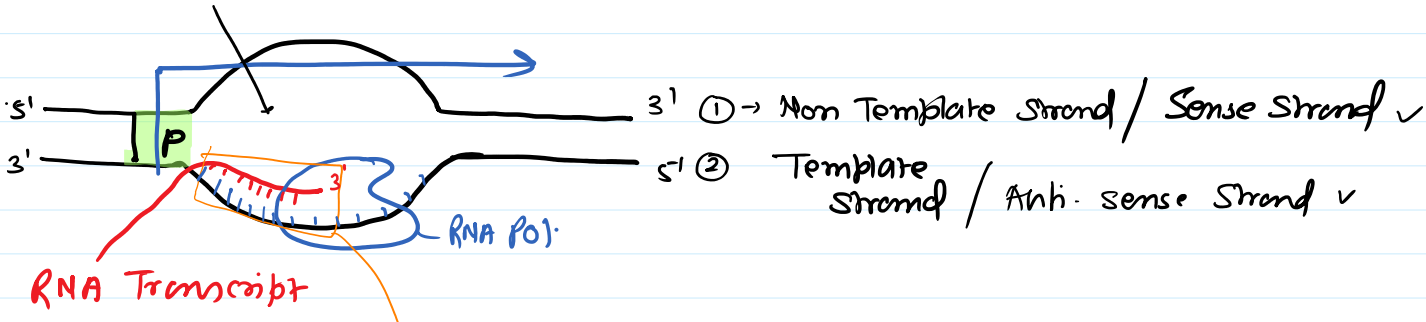
Types of RNA ⇒

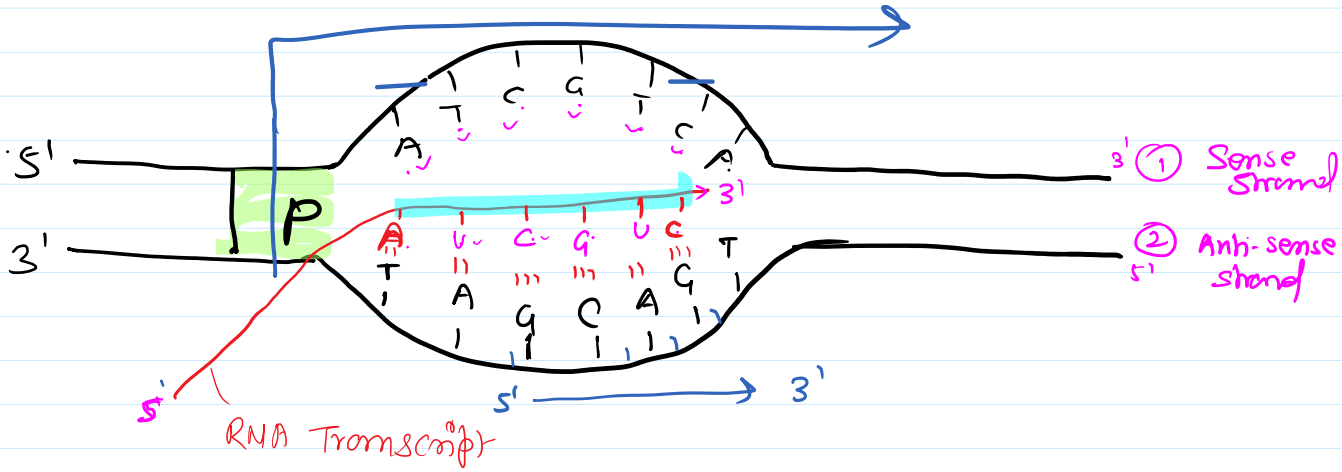
- Sn RNA
- mi RNA
- Sno RNA
- g RNA
- hn RNA
- mRNA → messenger RNA
- t RNA
- Sc RNA
- rRNA → most Abundant in Nucleus

Transcription

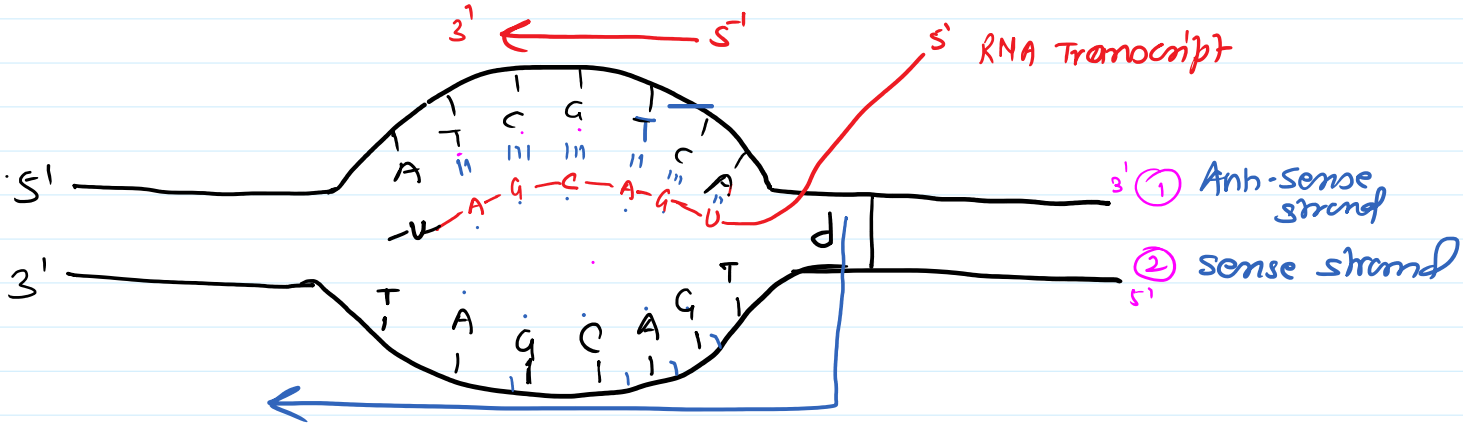
1. Template dependent process
2. Direction of Synthesis is 5' → 3'
3. Start Site → Promoter

Transcription Bubble [10-12 nt]





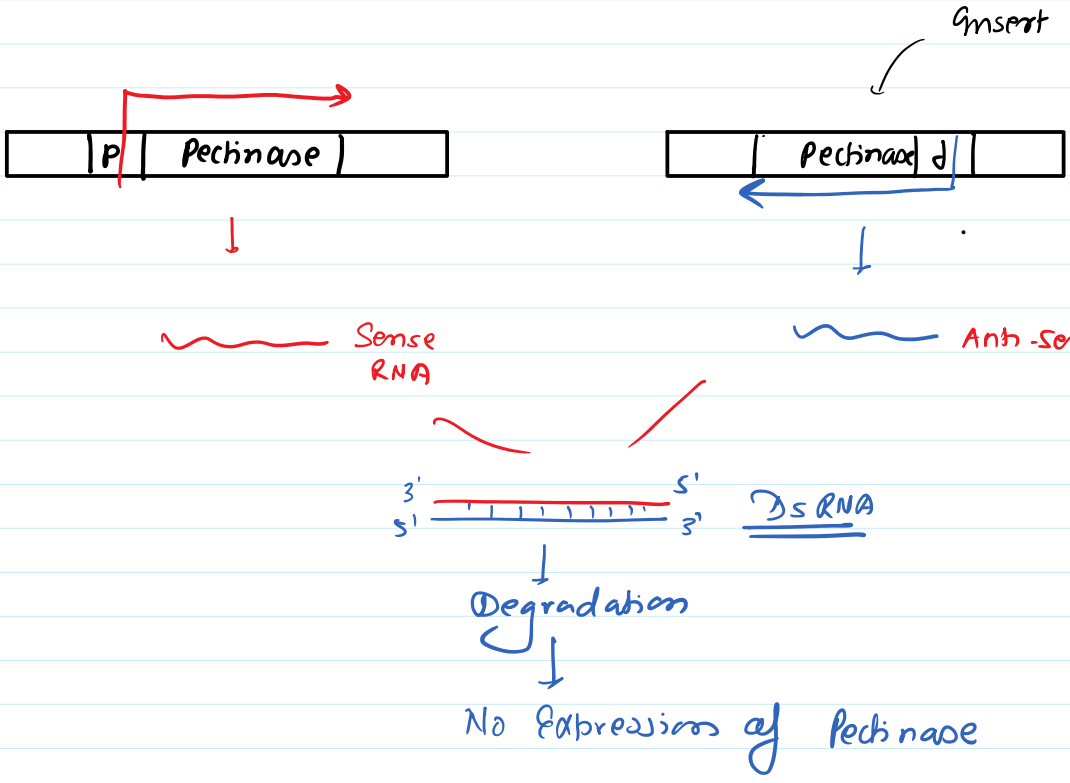
Promoter orientation determines the sense and Anti-sense Strand



* In Gene Silencing – Promoter orientation play important Role

eg. Flavor-saver Tomato

Insert



Pectinase gene Silencing by using Anti-sense RNA tech.

Transcription

- Sense Strand → 5' ⟶ 3'
- Antisense → 3' ⟶ 5'
- RNA Transcript → 5' ⟶ 3' (Direction of Transcription)

Enzymes -

- DNA Dependent RNA Polymerase

Substrate

- NTPs (Ribonucleotides / Ribonucleoside Tri phosphate)

Ribonucleoside = Sugar + N. Base

Ribonucleotide = Sugar + N. Base + (P)

→ ATP, CTP, GTP, UTP

✱ Transcription

- Direction → 5' → 3'
- Template Required
- RNA Pol.
- NTPs used as substrate
- Transcription Rate = 40 nt/sec
- Ds DNA melting start at Promoter site
  - Formation of Transcription bubble (10-12 nt)
    - RNA Transcript – 6-8 nt RNA DNA Hybrid formation
    - RNA Polymarase
      - 5' → 3' Polymarase activity +ve
      - 5' ← 3' Exonuclease activity –ve

Error Rate = $\frac{1}{10,000}$

Length of RNA is < 10 Kb [the chance of error is very low]

if there is error during Transcription:

Proof Reading-

(i) Pyrophosphate Editing

(ii) Hydrolytic Cleavage

RNA Polymarase

o Prokaryotic RNA Polymerase

- Single Enzyme with multiple Subunit

Codes : mRNA
rRNA
tRNA

$\alpha_2, \beta, \beta', \omega$ + σ

↓

Apo Enzyme

↓

Holo Enzyme

σ Subunit

- σ^{28} → Flagellar Protein Expression → during Chemotaxis
- σ^{70} → Normal gene Expression
- σ^{54} → in N_2 metabolism or Nif gene Expression
- σ^{32} → Heat Shock Protein Expression
- σ^{s} → Sporulation
- σ^{38} → Stationary Phase

* In Presence of σ Factor RNA Polymerase has 10000 folds more affinity for Promoter

E. coli - RNA Polymerase

↓

α, α'] Low Affinity with Promoter

β' Holds template

β - Catalytic RNA Pol. [Initiation & Elongation]
↳ Contain Polymerase activity.

ω - assembly of RNA Polymerase

if α Subunit → ADP ribosylation

↓

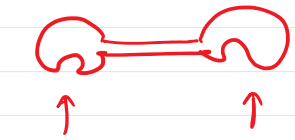
α - can not binds with Promoter

if β' is treated with Heparin (-vely charged)

↓

β' can not hold template (DNA - vely charged)

β Subunit →



↑ Initiation — T — Rifamycine

↑ Elongation — T — • Actinomycine D, • Streptolydigin

* Actinomycine D - is an inhibitor of Both Prokaryotic and Eukaryotic RNA Polymerase

→ RNA Pol. Required mg^{++} ion as co-factor for Catalytic Role

Eukaryotic RNA Polymerase

• Transcription Rate = $G_1 > G_2 > S >> M$

RNA Polymerase

(i) RNA Pol. I - rRNA [28SrRNA, 5.8SrRNA, 18SrRNA]

(ii) RNA Pol. II - mRNA, SnRNA, SnoRNA, miRNA

gmRNA, SiRNA

(iii) RNA Pol. III - tRNA, 5S, rRNA U6 snRNA

In Plants

- RNA Pol. IV and V are also +nt.
- involve in Synthesis of miRNA
- miRNA
  - Chromatin Remodelling
  - gene Silencing
  - Epigenetic Change

Inhibitors

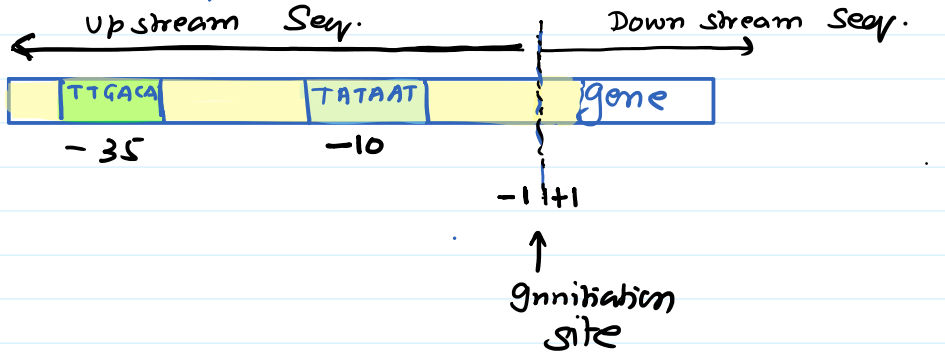
RNA Pol. II → highly sensitive with α amanitin

RNA Pol. I → insensitive " " "

RNA Pol. III → less sensitive " "

Transcriptional promoter

- K/a Transcription start site
- during Transcription RNA Pol. Binds with promoter seq.



-10 Seq.]
-35 Seq.] → Consensus Seq.

- Similar seq. +nt in almost all promoter

in Concensus seq. Generally variation is not allowed but small variation can be observed

- if there is variation in seq. — promoter become weak

Difference b/w Concensus and Conserved seq.

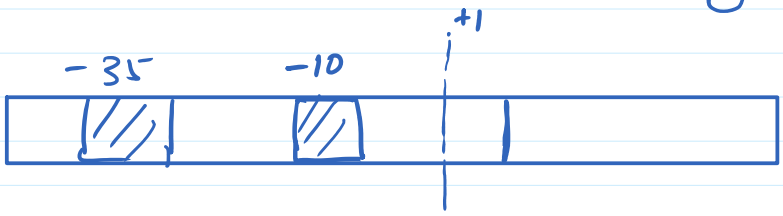
→ Consensus seq.	Conserved seq.
- small variation can be seen in different individual	- variation is not allowed

TA TA AT - 10 seq or ise k/a Pribnow box in E. coli

82.1. 89.1. 52.1. 59.1. 49.1. 89.1.] .·. occurance

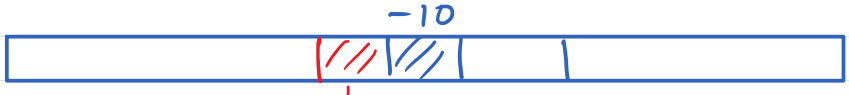
* if there is change in Consensus seq. promoter become weak -

* Bacterial promoter is generally strong promoter



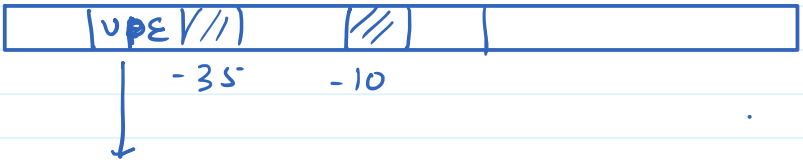
Strong promoter

if only -10 seq. is not → k/a weak promoter



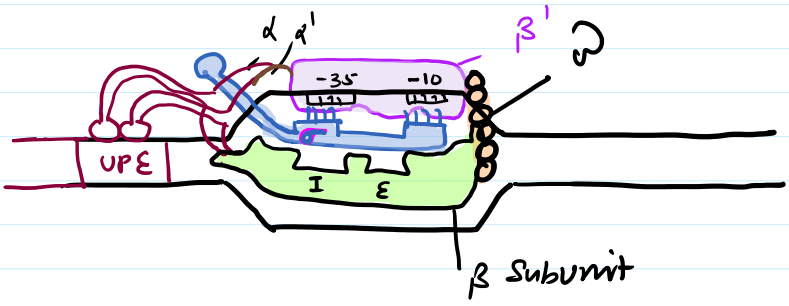
→ Strong promoter

Extended -10 seq.



Up Element

- Helps in Recruitment of RNA POL.
- α- C-Terminal Domain of RNA POL. - Recognize (α-CTD) UP-Element



Assembly of RNA POL.